```
=> fil reg; d que l2
FILE 'REGISTRY' ENTERED AT 15:52:41 ON 14 APR 2004
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES:   13 APR 2004  HIGHEST RN 675103-21-6
DICTIONARY FILE UPDATES:  13 APR 2004  HIGHEST RN 675103-21-6

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2004

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Crossover limits have been increased.  See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html


L2            30 SEA FILE=REGISTRY ABB=ON  E[QSHYE][SQITNP][FTSPLI][NSKMTP][DKTE
                 ][FLRI][TSN]R[IVA]/SQSP


=> d rn cn sql kwic nte lc 1-30 l2

L2   ANSWER 1 OF 30  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   654766-87-7  REGISTRY  -Use Registry # to match sequence to citation
CN   Protein (Rhodopseudomonas palustris clone US20030233675-SEQID-20641) (9CI)
     (CA INDEX NAME)
OTHER NAMES:
CN   641: PN: US20030233675 SEQID: 20641 claimed protein
SQL  345
SQL = sequence length
SEQ      51 RVIENQGLFW KLALNGIILN TRPARKAKDY QKIWNHEKNE SPLKTITRAQ
                                                    = =========

HITS AT:  90-99

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS

L2   ANSWER 2 OF 30  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   626155-11-1  REGISTRY
CN   Ferrochelatase (Rhodopseudomonas palustris CGA009 strain CGA009 gene hemZ)
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank CAE26319
CN   GenBank CAE26319 (TRANSLATED FROM: GenBank BX572595)
SQL  345

SEQ      51 RVIENQGLFW KLALNGIILN TRPARKAKDY QKIWNHEKNE SPLKTITRAQ
                                                    = =========

HITS AT:  90-99

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS

L2   ANSWER 3 OF 30  REGISTRY  COPYRIGHT 2004 ACS on STN
```

RN 626113-69-7 REGISTRY
CN Protein (Bdellovibrio bacteriovorus strain HD100 292-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAE78991
CN GenBank CAE78991 (TRANSLATED FROM: GenBank BX842648)
SQL 292

SEQ 201 VNGVLAYALE KTDYERNNIA VPPLKFLKVK NMPNHISVWA SCEKSLRGEQ

SEQ 251 ILKDLTRAVR EKNVKGKIYK YFMQELPPDM KKGYRALYDT PP

HITS AT: 249-258
LC STN Files: CA, CAPLUS

L2 ANSWER 4 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 623719-21-1 REGISTRY
CN GenBank CAD54412 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAD54412 (TRANSLATED FROM: GenBank AJ511870)
SQL 1726

SEQ 101 LCNYVFSAHC GDAYEDFNIQ LRRVQESNTT TLSRVTMKLD GLVVELTKSS

HITS AT: 126-135
LC STN Files: CAPLUS

L2 ANSWER 5 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 602352-27-2 REGISTRY
CN Protein (Methanopyrus kandleri strain AV19 gene MK1614) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1613: PN: WO03076575 SEQID: 1614 claimed sequence
SQL 157

SEQ 1 MAEKKNEQEI QQELQRLIAE INRLQGQMEA INAQIDLIES SISELNRVEE

HITS AT: 39-48

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 6 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 573581-39-2 REGISTRY
CN ABC transporter, periplasmic sugar-binding protein (Chromobacterium violaceum strain ATCC 12472 gene CV0262) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAQ57941
CN GenBank AAQ57941 (Translated from: GenBank AE016910)
SQL 415

SEQ 251 LAMLESTPTT LTRVRDEAPK VYRDTRVAAA PLGPTGIAAG GWMFNFAVAK

HITS AT: 255-264
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 7 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 570464-44-7 REGISTRY
CN Protein (Proteus mirabilis strain ATCC202157 clone US6605709-SEQID-7333 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3161: PN: US6605709 SEQID: 7333 claimed protein
SQL 254

SEQ 51 ITSTRTALGK GLFEISVKKE NIGIAIQILE EYQLPTISRI EITQLFPSDA

HITS AT: 81-90
LC STN Files: CA, CAPLUS

L2 ANSWER 8 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 549605-92-7 REGISTRY
CN 2217: PN: WO03008540 SEQID: 8061 unclaimed protein (9CI) (CA INDEX NAME)
SQL 430

SEQ 351 QQQKVAFLFC CGCSMCEETL TDRNRVKKAQ QYHLPTPNRI SGLETSHRRT

HITS AT: 367-376
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 9 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 524076-00-4 REGISTRY
CN 10: PN: US6566583 SEQID: 10 unclaimed protein (9CI) (CA INDEX NAME)
SQL 543

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF

HITS AT: 30-39

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 10 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 510915-30-7 REGISTRY
CN Protein (Propionibacterium acnes strain ATCC6919 clone
WO03033515-SEQID-27954 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3954: PN: WO03033515 SEQID: 27954 claimed protein
SQL 113

SEQ 51 APNSTAFCRS PVSIRPATRP AAKESPPPTR SRISRLGRST ERTKPVSFDH

HITS AT: 74-83

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 11 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 510901-64-1 REGISTRY
CN Protein (Propionibacterium acnes strain ATCC6919 clone
WO03033515-SEQID-26541 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2541: PN: WO03033515 SEQID: 26541 claimed protein
SQL 79

SEQ 1 TIEVSPGVVM ARAPWAAPNS TAFCRSPVSI RPATRPAAKE SPPPTRSRIS

HITS AT: 40-49

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 12 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 489862-35-3 REGISTRY
CN GenBank CAA58438 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAA58438 (Translated from: GenBank X83413)

SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV

HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 13 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 485104-00-5 REGISTRY
CN GenBank AAA46012 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAA46012 (Translated from: GenBank M87287)
SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV

HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 14 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 483502-77-8 REGISTRY
CN GenBank BAB17787 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAB17787 (Translated from: GenBank AB042530)
SQL 1851

SEQ 101 YFPGLCNYVF SEHCGAAYED FNIQLRRGLE SNSTTLSRVI MKLDGLVVEL

HITS AT: 130-139
NTE

type	------ location ------		description
uncommon	Aaa-1846	-	-

L2 ANSWER 15 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 459531-51-2 REGISTRY
CN GenBank AAB81126 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAB81126 (Translated from: GenBank U73935)
SQL 543

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF

HITS AT: 30-39

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 16 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 432279-88-4 REGISTRY
CN Protein (Propionibacterium acnes strain ATCC6919 clone WO0181581-SEQID-27954 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2954: PN: WO0181581 SEQID: 27954 claimed protein
SQL 113

SEQ 51 APNSTAFCRS PVSIRPATRP AAKESPPPTR SRISRLGRST ERTKPVSFDH

HITS AT: 74-83

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 17 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 432266-21-2 REGISTRY
CN Protein (Propionibacterium acnes strain ATCC6919 clone WO0181581-SEQID-26541 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1541: PN: WO0181581 SEQID: 26541 claimed protein
SQL 79

SEQ 1 TIEVSPGVVM ARAPWAAPNS TAFCRSPVSI RPATRPAAKE SPPPTRSRIS

HITS AT: 40-49

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 18 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 406671-25-8 REGISTRY
CN Prefoldin, molecular chaperone implicated in de novo protein folding (Methanopyrus kandleri strain AV19 gene GIM5) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAM02827
CN GenBank AAM02827 (Translated from: GenBank AE010451)
SQL 157

SEQ 1 MAEKKNEQEI QQELQRLIAE INRLQGQMEA INAQIDLIES SISELNRVEE

HITS AT: 39-48

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 19 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 353881-58-0 REGISTRY
CN Galactose-1-phosphate uridyltransferase (Clostridium acetobutylicum strain ATCC 824 gene CAC2961) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK80903
CN GenBank AAK80903 (Translated from: GenBank AE007793)
SQL 497

SEQ 201 LNKSKWFLQY SPYTYYNEHC IILNNEHIPM KISRITFENL LSFIDILPHY

HITS AT: 226-235
LC STN Files: CA, CAPLUS

L2 ANSWER 20 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 348670-68-8 REGISTRY
CN Protein (Sulfolobus solfataricus gene SSO2259) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAK42425
CN GenBank AAK42425 (Translated from: GenBank AE006830)
SQL 220

SEQ 101 KGILDPIIGL LEDEESLGKI INALINDFTL NLINHWEEII NDLSRIDLTN

HITS AT: 137-146
LC STN Files: CA, CAPLUS

L2 ANSWER 21 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 342056-52-4 REGISTRY

CN Protein (Shewanella putrefaciens 542-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: JP2001145490 SEQID: 13 claimed protein
SQL 542

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF

HITS AT: 30-39
LC STN Files: CA, CAPLUS

L2 ANSWER 22 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 325762-37-6 REGISTRY
CN Blood-coagulation factor X, prepro-[227-serine,228-glutamine,229-threonine,230-serine,231-lysine,232-leucine,233-threonine] (human liver) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 8: PN: WO0110896 SEQID: 2 claimed protein
SQL 488

SEQ 201 KPYDAADLDP TENPFDLLDF NQTQPESQTS KLTRIVGGQE CKDGECPWQA

HITS AT: 226-235
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 23 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 325762-36-5 REGISTRY
CN Blood-coagulation factor X, prepro-[227-glutamine,228-serine,229-phenylalanine,230-asparagine,231-aspartic acid,232-phenylalanine,233-threonine] (human liver) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: WO0110896 SEQID: 2 claimed protein
SQL 488

SEQ 201 KPYDAADLDP TENPFDLLDF NQTQPEQSFN DFTRIVGGQE CKDGECPWQA

HITS AT: 226-235
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 24 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 303239-87-4 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173674) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1354: PN: EP1033405 SEQID: 66354 claimed protein
SQL 151

SEQ 1 MPCSSDHEAW MKCYKENIGS PLKCSGFVKS FQDCARRSRQ QVNPEENSNT

51 LNRVNLGEQI FLSIFNVMTR MMLGAIVEEE ERTILGNELK KLILLFQISK

HITS AT: 45-54
LC STN Files: CA, CAPLUS

L2 ANSWER 25 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 303239-86-3 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173673) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1353: PN: EP1033405 SEQID: 66353 claimed protein
SQL 217

SEQ 101 ARRSRQQVNP EENSNTLNRV NLGEQIFLSI FNVMTRMMLG AIVEEEERTI

HITS AT: 111-120
LC STN Files: CA, CAPLUS

L2 ANSWER 26 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 303239-85-2 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2173672) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1352: PN: EP1033405 SEQID: 66352 claimed protein
SQL 274

SEQ 151 VKSFQDCARR SRQQVNPEEN SNTLNRVNLG EQIFLSIFNV MTRMMLGAIV

HITS AT: 168-177
LC STN Files: CA, CAPLUS

L2 ANSWER 27 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 167975-38-4 REGISTRY
CN Phosphoprotein (human herpesvirus 6 strain U1102 gene U11) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Phosphoprotein (human herpes virus 6 strain U1102 gene U11)
SQL 870

SEQ 101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV

HITS AT: 120-129

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 28 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 153926-89-7 REGISTRY
CN Protein (Shewanella putrefaciens clone pEPA 543-amino acid reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein (Shewanella putrefaciens strain SCRC-2874 open reading frame ORF9)
CN Protein (Shewanella tumefaciens clone pEPA open reading frame ORF9)
SQL 543

SEQ 1 MNPTATNEML SPWPWAVTES NISFDVQVME QQLKDFSRAC YVVNHADHGF

HITS AT: 30-39

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 29 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 153676-37-0 REGISTRY
CN Protein (human herpesvirus 6 strain U1102 gene P1LF1) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Protein (human herpes virus 6 strain U1102 gene P1LF1)
OTHER NAMES:
CN GenBank AAA16716
CN GenBank AAA16716 (Translated from: GenBank L25528)
SQL 871

SEQ 101 NSKGLNKGIF ENMFTNKEKF ESQFSDINRA LLRLGNFIKW GSNVAIDTPY

HITS AT: 121-130
LC STN Files: CA, CAPLUS

L2 ANSWER 30 OF 30 REGISTRY COPYRIGHT 2004 ACS on STN
RN 147156-14-7 REGISTRY
CN Protein p 100 (human herpesvirus 6 clone pDF446-4/pDF446-3/pD2Hae/pMF101R)

```
     (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Protein p 100 (human herpes virus 6 clone pDF446-4/pDF446-
     3/pD2Hae/pMF101R)
OTHER NAMES:
CN   P100 capsid protein (human herpesvirus 6)
SQL  869

SEQ    101 SKGLNKGIFE NMFTNKEKFE SQFSDINRAL LRLGNFIKWG SNVAIDTPYV

HITS AT:  120-129
LC   STN Files:   CA, CAPLUS, MEDLINE, TOXCENTER, USPATFULL


=> fil capl uspatf medl toxcenter; s l2
FILE 'CAPLUS' ENTERED AT 15:54:21 ON 14 APR 2004
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FILE 'USPATFULL' ENTERED AT 15:54:21 ON 14 APR 2004
CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'MEDLINE' ENTERED AT 15:54:21 ON 14 APR 2004

FILE 'TOXCENTER' ENTERED AT 15:54:21 ON 14 APR 2004
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L4            44 L2

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5            33 DUP REM L4 (11 DUPLICATES REMOVED)
                 ANSWERS '1-28' FROM FILE CAPLUS
                 ANSWERS '29-31' FROM FILE USPATFULL
                 ANSWERS '32-33' FROM FILE MEDLINE

=> d ibib ed ab hitrn 1-31; d iall 32-33

L5   ANSWER 1 OF 33  CAPLUS  COPYRIGHT 2004 ACS on STN DUPLICATE 1
ACCESSION NUMBER:         2003:326611  CAPLUS
DOCUMENT NUMBER:          138:298927
TITLE:                    Propionibacterium acnes genes and encoded protein
                          sequences and their use in therapy and diagnosis of
                          acne vulgaris
INVENTOR(S):              Mitcham, Jennifer L.; Skeiky, Yasir A. W.; Persing,
                          David H.; Bhatia, Ajay; Maisonneuve, Jean-Francois L.;
                          Zhang, Yanni; Wang, Siqing; Jen, Shyian; Lodes,
                          Michael J.; Benson, Darin R.; Jones, Robert; Carter,
                          Darrick; Barth, Brenda; Vallieve-Douglass, John
PATENT ASSIGNEE(S):       Corixa Corporation, USA
SOURCE:                   PCT Int. Appl., 1481 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   8
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
     WO 2003033515      A1   20030424      WO 2002-XF32727  20021011
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
```

CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US,
UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG

WO 2003033515 A1 20030424 WO 2002-US32727 20021011
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,
RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US,
UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-978825 A 20011015
WO 2002-US32727 A 20021011

ED Entered STN: 30 Apr 2003

AB Compns. and methods for the therapy and diagnosis of acne vulgaris and other related conditions are disclosed. The invention provides 299 contig sequences assembled from 56,716 fragments of the Propionibacterium acnes (strain ATCC 6919 or NCTC737) genome. Translation of all 299 contigs in all 6 possible reading frames identified 28,913 open reading frames at least 50 amino acids in length. BLAST and GenMark bioinformatic analyses were used to identify protein-coding regions from the DNA sequence. Re-anal. using Phrap reduced the no. of contigs to 105, and identified 26,462 ORFs including an addnl. 1692 new putative ORFs. Several P. acnes antigens were identified by serol. expression cloning to be correlated with patients with histories of severe acnes. Given the importance of proteins as immunotherapeutic/vaccine targets, BLASTp and TBLASTN searches identified specific ORFs as members of the classes of transferase, enterotoxin, lipoprotein, membrane, permease, enterobactin, protease/proteinase, protein A, secreted, dismutase, adhesin, transporter, hemolysin, penicillin-binding protein, sialidase, siderophore, and lipase proteins. Therapeutic compns. may comprise one or more Propionibacterium acnes proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic compn. may comprise an antibody that binds a Propionibacterium acnes protein, antigen-presenting cell that expresses a Propionibacterium acnes protein, or a T cell that is specific for cells expressing such a protein. Such compns. may be used, for example, for the prevention and/or treatment of acne. An animal model for P. acnes-induced inflammatory acne is also provided for identification of immunogenic proteins by serol. expression cloning and proteomic anal. [This abstr. record is one of eight records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **510901-64-1 510915-30-7** use Registry # to match citation to sequence
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; Propionibacterium acnes genes and encoded protein sequences and their use in therapy and diagnosis of acne vulgaris)

L5 ANSWER 2 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2003:539800 CAPLUS
DOCUMENT NUMBER: 139:64475
TITLE: Abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant

INVENTOR(S): Kreps, Joel; Briggs, Steven P.; Cooper, Bret; Glazebrook, Jane; Goff, Stephen A.; Katagiri, Fumiyaki; Moughamer, Todd; Provart, Nicholas; Ricke, Darrell; Zhu, Tong
PATENT ASSIGNEE(S): Syngenta Participations AG, Switz.
SOURCE: PCT Int. Appl., 177 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003008540	A2	20030130	WO 2002-XA19668	20020621
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2003008540	A2	20030130	WO 2002-US19668	20020621
WO 2003008540	A3	20031204		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003135888	A1	20030717	US 2002-259165	20020926
US 2004010815	A1	20040115	US 2002-259194	20020926
US 2004016025	A1	20040122	US 2002-260238	20020926

PRIORITY APPLN. INFO.:		
US 2001-300112P	P	20010622
US 2001-314662P	P	20010824
US 2001-325277P	P	20010926
US 2001-332132P	P	20011121
WO 2002-US19668	A	20020621
US 2001-325448P	P	20010926
US 2002-368327P	P	20020327
US 2002-370620P	P	20020404
US 2002-370743P	P	20020404

ED Entered STN: 15 Jul 2003

AB Abiotic stress responsive polynucleotides and polypeptides are disclosed. Also disclosed are vectors, expression cassettes, host cells, and plants contg. such polynucleotides. Also provided are methods for using such polynucleotides and polypeptides, for example, to alter the responsiveness of a plant to abiotic stress. Rice (Oryza sativa japonica) cDNA library was constructed and sequenced, and used in GeneChip std. protocol for expression profiling of stress-regulated genes. Based on the profiles, clusters of nucleic sequences that were altered at least two-fold in response to the stress condition were identified. Identification of abiotic stress responsive genes using yeast two hybrid system was also demonstrated. Rice orthologs of Arabidopsis abiotic stress genes were identified by reverse genetics. Transgenic rice expressing "abiotic stress candidate gene" was produced. The present invention claimed

abiotic stress responsive cDNAs (SEQ IDs 1-4131, 8263-8353, 8445-8829 and 17505-17506) and proteins (SEQ IDs 4132-8262, 8354-8444, and 8830-9214), but the Sequence Listing was not made available on publication of the patent application.

IT **549605-92-7**
RL: PRP (Properties)
(unclaimed protein sequence; abiotic stress responsive polynucleotides and polypeptides from plants and methods of altering the stress responsiveness of a plant)

L5 ANSWER 3 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2003:390870 CAPLUS
DOCUMENT NUMBER: 138:380503
TITLE: Protein and cDNA sequences of a Schizochytrium aggregatum polyketide-like synthase (PKS-like) gene and use
INVENTOR(S): Facciotti, Daniel; Metz, James George; Lassner, Michael
PATENT ASSIGNEE(S): USA
SOURCE: U.S., 261 pp., Cont.-in-part of U.S. 6,140,486.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6566583	B1	20030520	US 1999-231899	19990114
US 6140486	A	20001031	US 1998-90793	19980604
CA 2359629	AA	20000720	CA 2000-2359629	20000114
WO 2000042195	A2	20000720	WO 2000-US956	20000114
WO 2000042195	A3	20000928		
W: BR, CA, IL, JP, MX				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1147197	A2	20011024	EP 2000-904357	20000114
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 2000008760	A	20021008	BR 2000-8760	20000114
JP 2002534123	T2	20021015	JP 2000-593752	20000114
US 2002194641	A1	20021219	US 2002-124800	20020416
US 2003101486	A1	20030529	US 2002-331061	20021227

PRIORITY APPLN. INFO.:

US 1997-48650P	P	19970604
US 1998-90793	A2	19980604
US 1999-231899	A	19990114
WO 2000-US956	W	20000114
US 2001-284066P	P	20010416
US 2001-298796P	P	20010615
US 2001-323269P	P	20010918

ED Entered STN: 22 May 2003
AB The present invention provides protein and cDNA sequences of a novel Schizochytrium aggregatum polyketide-like synthesis (PKS-like) gene. The present invention relates to compns. and methods for prepg. poly-unsatd. long chain fatty acids in plants, plant parts and plant cells, such as leaves, roots, fruits and seeds. Nucleic acid sequences and constructs encoding PKS-like genes required for the poly-unsatd. long chain fatty acid prodn., including the genes responsible for eicosapentenoic acid prodn. of Shewanella putrefaciens and novel genes assocd. with the prodn. of docosahexaenoic acid in Vibrio marinus are used to generate transgenic plants, plant parts and cells which contain and express one or more transgenes encoding one or more of the PKS-like genes assocd. with such long chain polyunsatd. fatty acid prodn. Expression of the PKS-like genes

in the plant system permits the large scale prodn. of poly-unsatd. long chain fatty acids such as eicosapentenoic acid and docosahexaenoic acid for modification of the fatty acid profile of plants, plant parts and tissues. Manipulation of the fatty acid profiles allows for the prodn. of com. quantities of novel plant oils and products.

IT **524076-00-4**
RL: PRP (Properties)
(unclaimed protein sequence; protein and cDNA sequences of a Schizochytrium aggregatum polyketide-like synthase (PKS-like) gene and use)

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2003:816565 CAPLUS
DOCUMENT NUMBER: 139:287120
TITLE: The complete genome sequence of Chromobacterium violaceum reveals remarkable and exploitable bacterial adaptability
AUTHOR(S): Ribeiro de Vasconcelos, Ana Tereza; de Almeida, Darcy F.; Hungria, Mariangela; Guimaraes, Claudia Teixeira; Antonio, Regina Vasconcellos; Almeida, Francisca Cunha; de Almeida, Luiz G. P.; de Almeida, Rosana; Alves-Gomes, Jose Antonio; Andrade, Elizabeth Mazoni; Araripe, Julia; Florencio de Araujo, Magnolia Fernandes; Astolfi-Filho, Spartaco; Azevedo, Vasco; Baptista, Alessandra Jorge; Bataus, Luiz Artur Mendes; Batista, Jacqueline da Silva; Belo, Andre; van den Berg, Cassio; Bogo, Mauricio; Bonatto, Sandro; Bordignon, Juliano; Brigido, Marcelo Macedo; Brito, Cristiana Alves; Brocchi, Marcelo; Burity, Helio Almeida; Camargo, Anamaria Aranha; Cardoso, Divina das Dores de Paula; Carneiro, Newton Portilho; Carraro, Dirce Maria; Carvalho, Claudia Marcia Benedetto; Cascardo, Julio Cezar de Mattos; Cavada, Benildo Sousa; Chueire, Ligia Maria O.; Creczynski-Pasa, Tania Beatriz; Costa da Cunha, Nivaldo, Jr.; Fagundes, Nelson; Falcao, Clarissa Lima; Fantinatti, Fabiana; Farias, Izeni Pires; Felipe, Maria Sueli Soares; Ferrari, Lilian Pereira; Ferro, Jesus Aparecido; Ferro, Maria Ines Tiraboschi; Franco, Gloria Regina; Aguiar de Freitas, Nara Suzy; Furlan, Luiz Roberto; Gazzinelli, Ricardo Tostes; Gomes, Eliane Aparecida; Goncalves, Pablo Rodrigues; Grangeiro, Thalles Barbosa; Grattapaglia, Dario; Grisard, Edmundo Carlos; Hanna, Ebert Seixas; Silvia Neto, Jardim; Laurino, Jomar; Leoi, Lelia Cristina Tenorio; Lima, Lucymara Fassarella Agnez; Loureiro, Maria de Fatima; Pereira de Lyra, Maria do Carmo Catanho; Madeira, Humberto Maciel Franca; Manfio, Gilson Paulo; Maranhao, Andrea Queiroz; Martins, Wellington Santos; Zingaretti di Mauro, Sonia Marli; Batistuzzo de Medeiros, Silvia Regina; Meissner, Rosely de Vasconcellos; Moreira, Miguel Angelo Martins; Ferreira do Nascimento, Fabricia; Nicolas, Marisa Fabiana; Oliveira, Jaquelline Germano; Oliveira, Sergio Costa; Paixao, Roger Ferreira Cury; Parente, Juliana Alves; Pedrosa, Fabio de Oliveira; Pena, Sergio Danilo Junho; Pereira, Jose Odair; Pereira, Maristela; Pinto, Luciana Santos Rodrigues Costa; Pinto, Luciano da Silva; Porto, Jorge Ivan Rebelo; Potrich, Deise Porto; Ramalho-Neto, Cicero Eduardo; Reis, Alessandra Maria Moreira; Rigo, Liu Um; Rondinelli, Edson; Pedraca do Santos, Elen

Bethleen; Santos, Fabricio R.; Schneider, Maria Paula Cruz; Seuanez, Hector N.; Silva, Ana Maria Rodrigues; Luiz da Costa da Silva, Artur; Silva, Denise Wanderlei; Silva, Rosane; Simoes, Isabella de Carmo; Simon, Daniel; Soares, Celia Maria de Almeida; Soares, Renata de Bastos Ascenco; Souza, Emanuel Maltempi; Lobo de Souza, Kelly Rose; Souza, Rangel Celso; Steffens, Maria Berenice Reynaud; Steindel, Mario; Teixeira, Santuza Ribeiro; Urmenyi, Turan; Vettore, Andre; Wassem, Roseli; Zaha, Arnaldo; Simpson, Andrew John George

CORPORATE SOURCE: Labinfo, Laboratorio Nacional de Computacao Cientifica/Ministerio da Ciencia e Tecnologia, Petropolis, CEP 25651-071, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2003), 100(20), 11660-11665
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 17 Oct 2003

AB Chromobacterium violaceum is one of millions of species of free-living microorganisms that populate the soil and water in the extant areas of tropical biodiversity around the world. The complete genome of C. violaceum consists of a single circular chromosome of 4,751,080 bp with an av. G+C content of 64.83% and 4431 uniformly distributed protein coding ORFs that cover 89% of the genome. Its complete genome sequence reveals (i) extensive alternative pathways for energy generation, (ii) .apprx.500 ORFs for transport-related proteins, (iii) complex and extensive systems for stress adaptation and motility, and (iv) widespread utilization of quorum sensing for control of inducible systems, all of which underpin the versatility and adaptability of the organism. The genome also contains extensive but incomplete arrays of ORFs coding for proteins assocd. with mammalian pathogenicity, possibly involved in the occasional but often fatal cases of human C. violaceum infection. There is, in addn., a series of previously unknown but important enzymes and secondary metabolites including paraquat-inducible proteins, drug and heavy-metal-resistance proteins, multiple chitinases, and proteins for the detoxification of xenobiotics that may have biotechnol. applications. The genome sequence is deposited in GenBank/EMBL/DDBJ under accession no. AE016825 and in the NCBI RefSeq Genome Database under accession no. NC_005085.

IT **573581-39-2**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Chromobacterium violaceum reveals remarkable and exploitable bacterial adaptability)

REFERENCE COUNT: 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

ACCESSION NUMBER: 2002:96396 CAPLUS
DOCUMENT NUMBER: 137:1520

TITLE: Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris

INVENTOR(S): Skeiky, Yasir A. W.; Persing, David H.; Mitcham, Jennifer L.; Wang, Siqing Steven; Bhatia, Ajay; L'Maisonneuve, Jean-Francois; Zhang, Yanni; Jen, Shyian; Carter, Darrick

PATENT ASSIGNEE(S): Corixa Corporation, USA

SOURCE: PCT Int. Appl., 1069 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001081581	A2	20011101	WO 2001-XE12865	20010420
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001081581	A2	20011101	WO 2001-US12865	20010420
WO 2001081581	A3	20020314		
WO 2001081581	C2	20030103		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:	US 2000-199047P	P	20000421
	US 2000-208841P	P	20000602
	US 2000-216747P	P	20000707
	WO 2001-US12865	W	20010420

ED Entered STN: 06 Feb 2002

AB Compns. and methods for the therapy and diagnosis of acne vulgaris and other related conditions are disclosed. Compns. may comprise one or more Propionibacterium acnes proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Thus, overlapping clones representing .apprx.8.6 full-length genome equiv. from a P. acnes genomic library were aligned to form 299 linear contigs. These 299 contigs represent a total assembled length of about 2,656,860 nucleotides covering >90% of the P. acnes genome. Six-frame translation is performed in order to predict 28,913 open reading frames encoding P. acnes polypeptide sequences .gtoreq.50 amino acids in length. A therapeutic compn. may also comprise an antibody that binds a P. acnes protein, antigen-presenting cells that express a P. acnes protein, or a T cell that is specific for cells expressing such a protein. Such compns. may be used, for example, for the prevention and/or treatment of acne.

IT **432266-21-2 432279-88-4**
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris)

L5 ANSWER 6 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6

ACCESSION NUMBER:	2001:115178 CAPLUS
DOCUMENT NUMBER:	134:168320
TITLE:	Factor X substitution mutant with an improved ability to be activated
INVENTOR(S):	Himmelspach, Michele; Schlokat, Uwe
PATENT ASSIGNEE(S):	Baxter A.-G., Austria
SOURCE:	PCT Int. Appl., 50 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001010896	A2	20010215	WO 2000-EP7631	20000807
WO 2001010896	A3	20020711		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AT 9901377	A	20020715	AT 1999-1377	19990810
AT 410216	B	20030325		
EP 1238065	A2	20020911	EP 2000-949465	20000807
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				

PRIORITY APPLN. INFO.: AT 1999-1377 A 19990810
WO 2000-EP7631 W 20000807
OTHER SOURCE(S): MARPAT 134:168320
ED Entered STN: 15 Feb 2001
AB The invention relates to factor Xa analogs with a modified protease cleavage site, comprising a substitution of a min. of one of the amino acid between Glu226 and Arg234 and possibly Ile235 in the region of activation peptide. These modified cleavage sites in the region of activation peptide change protease specificity and facilitate factor XIa cleavage of the precursor. The invention also relates to prepns. contg. said factor Xa analogs and methods for the prodn. thereof. The prepro-factor X analogs may be used to produce high-purity factor X for use as coagulants.
IT **325762-36-5P 325762-37-6P**
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; factor X substitution mutant with improved ability to be activated)

L5 ANSWER 7 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 1998:572263 CAPLUS
DOCUMENT NUMBER: 129:212504
TITLE: Genes coding for eicosapentaenoic acid synthetic enzymes and use for production of eicosapentaenoic acid in Escherichia coli
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: U.S., 81 pp., Cont.-in-part of U.S. 5,683,898.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5798259	A	19980825	US 1996-752929	19961120
US 5683898	A	19971104	US 1995-375709	19950120

PRIORITY APPLN. INFO.: JP 1992-147945 19920515
US 1994-178251 19940110
US 1995-375709 19950120

ED Entered STN: 08 Sep 1998

AB Claimed are DNA sequences encoding eicosapentaenoic acid (EPA) biosynthetic enzymes derived from Shewanella putrefaciens, and their cloning in Escherichia coli for the prodn. of EPA. There is provided an advantageous process for prodn. of EPA by a recombinant technique wherein genes coding for EPA biosynthesis enzymes useful as pharmaceuticals, agrochems., foods, feeds or the like are obtained from microorganisms. EPA is produced by obtaining genes coding for eicosapentaenoic acid (EPA) biosynthesis enzymes, constructing a plasmid by joining the genes to a vector, transforming E. coli with the plasmid, and culturing the transformed E. coli.

IT **153926-89-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genes coding for eicosapentaenoic acid synthetic enzymes and use for prodn. of eicosapentaenoic acid in E. coli)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8
ACCESSION NUMBER: 1997:719630 CAPLUS
DOCUMENT NUMBER: 128:10898
TITLE: Sequence of Shewanella putrefaciens gene coding for 9 eicosapentaenoic acid synthesizing enzymes and process for production of eicosapentaenoic acid with expression in Escherichia coli using pEPA vector
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: U.S., 77 pp., Cont.-in-part of U.S. Ser. No. 178,251, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5683898	A	19971104	US 1995-375709	19950120
US 5798259	A	19980825	US 1996-752929	19961120

PRIORITY APPLN. INFO.: JP 1992-147945 19920515
US 1994-178251 19940110
US 1995-375709 19950120

ED Entered STN: 14 Nov 1997

AB There is provided an advantageous process for prodn. of EPA by a gene recombinant technique wherein genes coding for biosynthesis enzymes for eicosapentaenoic acid (EPA) useful as pharmaceuticals, agrochems., foods, feeds or the like is obtained from microorganisms. EPA is produced by obtaining genes coding for eicosapentaenoic acid (EPA) biosynthesis enzymes, constructing a plasmid by joining the genes to a vector, transforming E. coli with the plasmid, and culturing the transformed E. coli.

IT **153926-89-7P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; Shewanella putrefaciens genes encoding eicosapentaenoic acid synthesizing enzymes and prodn. of eicosapentaenoic acid with Escherichia coli)

L5 ANSWER 9 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 10
ACCESSION NUMBER: 1993:210909 CAPLUS
DOCUMENT NUMBER: 118:210909
TITLE: Gene for the major antigenic structural protein (p100) of human herpesvirus 6
AUTHOR(S): Neipel, Frank; Ellinger, Klaus; Fleckenstein, Bernhard
CORPORATE SOURCE: Inst. Klin. Mol. Virol., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Germany
SOURCE: Journal of Virology (1992), 66(6), 3918-24
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 29 May 1993
AB A human herpesvirus 6 (HHV-6) structural protein of 100 kDa (p100) is the polypeptide most frequently and intensively reactive in immunoblotting analyses with human sera on HHV-6-infected cells or partially purified virions. The gene for p100 was identified by screening a bacteriophage lambda library with monospecific rabbit antisera. The gene codes for a polypeptide of 870 amino acids with a calcd. mol. size of 97 kDa. Its N-terminal third is weakly homologous to the immunogenic basic matrix phosphoprotein pp150 of human cytomegalovirus. Five fragments representing more than 93% of HHV-6 p100 were prokaryotically expressed. The antigenic epitopes of p100 were preliminarily mapped by immunoblotting with human sera. They are located within the C-terminal part which is neither homologous nor cross-reactive to pp150 of human cytomegalovirus. Availability of the gene for the immunodominant structural protein should provide tools for studies of pathogenesis by HHV-6.
IT **147156-14-7**
RL: PRP (Properties)
(amino acid sequence of, complete)

L5 ANSWER 10 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:68662 CAPLUS
DOCUMENT NUMBER: 140:158345
TITLE: A predator unmasked: Life cycle of Bdellovibrio bacteriovorus from a genomic perspective
AUTHOR(S): Rendulic, Snjezana; Jagtap, Pratik; Rosinus, Andrea; Eppinger, Mark; Baar, Claudia; Lanz, Christa; Keller, Heike; Lambert, Carey; Evans, Katy J.; Goesmann, Alexander; Meyer, Folker; Sockett, R. Elizabeth; Schuster, Stephan C.
CORPORATE SOURCE: Max-Planck-Institute for Developmental Biology, Tuebingen, 72076, Germany
SOURCE: Science (Washington, DC, United States) (2004), 303(5658), 689-692
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 28 Jan 2004
AB Predatory bacteria remain molecularly enigmatic, despite their presence in many microbial communities. The complete genome of Bdellovibrio bacteriovorus HD100, a predatory Gram-neg. bacterium that invades and consumes other Gram-neg. bacteria, is now reported. Its surprisingly large genome shows no evidence of recent gene transfer from its prey. A plethora of paralogous gene families coding for enzymes, such as hydrolases and transporters, are used throughout the life cycle of B. bacteriovorus for prey entry, prey killing, and the uptake of complex mols. The complete sequence comprising 3,782,950 bp and 3584 predicted open reading frames is deposited in GenBank/EMBL/DDBJ under accession no. BX842601 and in the RefSeq database under accession no. NC_005363.
IT **626113-69-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(amino acid sequence; life cycle of Bdellovibrio bacteriovorus based on its complete genomic sequence)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 11 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:146210 CAPLUS
TITLE: The mouse secreted gel-forming mucin gene cluster
AUTHOR(S): Escande, Fabienne; Porchet, Nicole; Bernigaud, Annie; Petitprez, Daniele; Aubert, Jean-Pierre; Buisine, Marie-Pierre
CORPORATE SOURCE: Unite 560 INSERM, Lille, 59045, Fr.
SOURCE: Biochimica et Biophysica Acta (2004), 1676(3), 240-250
CODEN: BBACAQ; ISSN: 0006-3002
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 23 Feb 2004
AB Using genomic cosmid and BAC clones and genome shotgun supercontigs available in GenBank, we detd. the complete gene structure of the four mouse secreted gel-forming mucin genes Muc2, Muc5ac, Muc5b and Muc6 and the organization of the genomic locus harboring these genes. The mouse secreted gel-forming mucin gene is 215 kb on distal chromosome 7 to 69.0 cM from the centromere and organized as: Muc6-Muc2-Muc5ac-Muc5b with Muc2, Muc5ac and Muc5b arranged in the same orientation and Muc6 in opposite. Mouse mucin genes have highly similar genomic organization to each other and to their resp. human homologues indicating that they have been well conserved through evolution. Deduced peptides showed striking sequence similarities in their N- and C-terminal regions whereas the threonine/serine/proline-rich central region is specific for each other and for species. Expression studies also showed that they have expression patterns similar to human mucin genes with Muc2 expressed in small and large intestines, Muc5ac and Muc6 in stomach, and Muc5b in laryngo-tracheal tract. These data constitute an important initial step for investigation of mucin gene regulation and mucin function through the use of animal models.
IT INDEXING IN PROGRESS
IT **623719-21-1**, GenBank CAD54412
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; mouse secreted gel-forming mucin gene cluster)
REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 12 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:5633 CAPLUS
DOCUMENT NUMBER: 140:158334
TITLE: Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris
AUTHOR(S): Larimer, Frank W.; Chain, Patrick; Hauser, Loren; Lamerdin, Jane; Malfatti, Stephanie; Do, Long; Land, Miriam L.; Pelletier, Dale A.; Beatty, J. Thomas; Lang, Andrew S.; Tabita, F. Robert; Gibson, Janet L.; Hanson, Thomas E.; Bobst, Cedric; Torres y Torres, Janelle L.; Peres, Caroline; Harrison, Faith H.; Gibson, Jane; Harwood, Caroline S.
CORPORATE SOURCE: Genome Analysis and Systems Modeling, Oak Ridge National Laboratory, Oak Ridge, TN, 37831, USA
SOURCE: Nature Biotechnology (2004), 22(1), 55-61
CODEN: NABIF9; ISSN: 1087-0156
PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 05 Jan 2004
AB Rhodopseudomonas palustris is among the most metabolically versatile bacteria known. It uses light, inorg. compds., or org. compds., for energy. It acquires carbon from many types of green plant-derived compds. or by carbon dioxide fixation, and it fixes nitrogen. This report describes the genome sequence of R. palustris, which consists of a 5,459,213-bp circular chromosome with 4836 predicted genes and a plasmid of 8427 bp. The sequence reveals genes that confer a remarkably large no. of options within a given type of metab., including three nitrogenases, five benzene ring cleavage pathways, and four light harvesting 2 systems. R. palustris encodes 63 signal transduction histidine kinases and 79 response regulator receiver domains. Almost 15% of the genome is devoted to transport. This genome sequence is a starting point to use R. palustris as a model to explore how organisms integrate metabolic modules in response to environmental perturbations. The genome sequence of R. palustris CGA009 ia available in GenBank/EMBL/DDBJ under accession nos. BX571963 (chromosome) and BX571964 (plasmid) and in the RefSeq database under accession no. NC_005296.
IT **626155-11-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris)
REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 13 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:737863 CAPLUS
DOCUMENT NUMBER: 139:256346
TITLE: The complete genome and protein sequence of the hyperthermophile Methanopyrus kandleri AV19 and monophyly of Archael methanogens, and methods of their use
INVENTOR(S): Slesarev, Alexei I.; Pavlov, Andrey; Pavlova, Nadezhda; Kozyavkin, Sergei
PATENT ASSIGNEE(S): Fidelity Systems, Inc., USA; Malykh, Andrei
SOURCE: PCT Int. Appl., 1023 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003076575	A2	20030918	WO 2003-US6664	20030304

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-361742P P 20020304
US 2002-380423P P 20020514
US 2002-410974P P 20020916
ED Entered STN: 19 Sep 2003

AB The complete 1,694,969 nucleotide sequence of the GC-rich genome of Methanopyrus kandleri was detd. using a novel approach. It is based on unlinking genomic DNA with the ThermoFidelase version of M. kandleri topoisomerase V and cycle sequencing directed by 2'-modified oligonucleotides (Fimers). Sequencing redundancy of 3.3-fold was sufficient to assemble the genome with <1 error per 40 kb. Using a combination of sequence database searches and coding potential prediction, 1692 protein-coding genes and 39 genes for structural RNAs were identified. M. kandleri proteins show an unusually high content of neg. charged amino acids, which might be an adaptation to its high intracellular salinity. Previous phylogenetic anal. of 16S RNA suggested that M. kandleri belonged to a very deep branch, close to the root of the archaeal tree. However, genome comparisons, using both trees constructed from concatenated alignments of ribosomal proteins and trees based on gene content, indicate that M. kandleri consistently groups with other archaeal methanogens. M. kandleri shares the set of genes implicated in methanogenesis and, in part, its operon organization with Methanococcus jannaschii and Methanothermobacter thermoautotrophicus. These findings indicate that archaeal methanogens are monophyletic. A distinctive feature of M. kandleri is the paucity of proteins involved in signaling and regulation of gene expression. Also, M. kandleri appears to have fewer genes acquired via lateral transfer than other archaea. These features might reflect the extreme habitat of this organism.

IT **602352-27-2**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; complete genome and protein sequence of hyperthermophile Methanopyrus kandleri AV19 and monophyly of Archael methanogens and methods of their use)

L5 ANSWER 14 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2004:11576 CAPLUS
DOCUMENT NUMBER: 140:158554
TITLE: Expression of microbial proteins in plants for production of plants with improved properties
INVENTOR(S): Cao, Yongwei; Hinkle, Gregory J.; Slater, Steven C.; Chen, Xianfeng; Goldman, Barry S.
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 122 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 12
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003233675	A1	20031218	US 2003-369493	20030220
PRIORITY APPLN. INFO.:			US 2002-360039P P	20020221

ED Entered STN: 08 Jan 2004
AB Recombinant constructs and methods useful for improvement of plants are provided. In particular, recombinant constructs comprising promoters functional in plant cells positioned for expression of polynucleotides encoding polypeptides from microbial sources are provided. The disclosed constructs and methods find use in prodn. of transgenic plants to provide plants, particularly crop plants, having improved properties. [This abstr. record is one of twelve records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **654766-87-7P**
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; expression of microbial proteins in plants for prodn. of plants with improved properties)

L5 ANSWER 15 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:629098 CAPLUS
DOCUMENT NUMBER: 139:145044
TITLE: Nucleic acid and amino acid sequences relating to Proteus mirabilis for diagnostics and therapeutics
INVENTOR(S): Breton, Gary L.
PATENT ASSIGNEE(S): Genome Therapeutics Corporation, USA
SOURCE: U.S., 870 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6605709	B1	20030812	US 2000-543681	20000405
US 6605709	B1	20030812	US 2000-543681	20000405

PRIORITY APPLN. INFO.: US 1999-128706P P 19990409
US 2000-543681 A 20000405

ED Entered STN: 15 Aug 2003
AB The invention provides isolated 4172 polypeptide and 4172 genomic DNA sequences derived from Proteus mirabilis strain 16525 (ATCC 202157). Chromosomal DNA was isolated after Zymolyase digestion and hydrodynamically sheared and the fragments of the genomic library sequenced and assembled. To identify P. mirabilis polypeptides, the compete genomic sequence of P. mirabilis was analyzed to identify all possible stop-to-stop open reading frames greater than 180 nucleotides in all 6 reading frames, the identified ORFs analyzed for homol. to known sequences, and the coding potential of non-homologous sequences evaluated with the program GENEMARK.RTM.. These sequences are useful in diagnosis and therapy of pathol. conditions, antibodies against the polypeptides, and methods for the prodn. of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathol. conditions resulting from bacterial infection. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
IT **570464-44-7**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acid and amino acid sequences relating to Proteus mirabilis for diagnostics and therapeutics)

L5 ANSWER 16 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:290302 CAPLUS
DOCUMENT NUMBER: 136:289776
TITLE: The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens
AUTHOR(S): Slesarev, Alexei I.; Mezhevaya, Katja V.; Makarova, Kira S.; Polushin, Nikolai N.; Shcherbinina, Olga V.; Shakhova, Vera V.; Belova, Galina I.; Aravind, L.; Natale, Darren A.; Rogozin, Igor B.; Tatusov, Roman L.; Wolf, Yuri I.; Stetter, Karl O.; Malykh, Andrei G.; Koonin, Eugene V.; Kozyavkin, Sergei A.
CORPORATE SOURCE: Fidelity Systems, Gaithersburg, MD, 20879, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2002), 99(7), 4644-4649
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 18 Apr 2002
AB The complete 1,694,969-nucleotide sequence of the GC-rich genome of Methanopyrus kandleri was detd. by using a whole direct genome sequencing approach. This approach is based on unlinking of genomic DNA with the ThermoFidelase version of M. kandleri topoisomerase V and cycle sequencing directed by 2'-modified oligonucleotides (Fimers). Sequencing redundancy (3.3-fold) was sufficient to assemble the genome with less than one error per 40 kb. Using a combination of sequence database searches and coding potential prediction, 1692 protein-coding genes and 39 genes for structural RNAs were identified. M. kandleri proteins show an unusually high content of neg. charged amino acids, which might be an adaptation to the high intracellular salinity. Previous phylogenetic anal. of 16S RNA suggested that M. kandleri belonged to a very deep branch, close to the root of the archaeal tree. However, genome comparisons indicate that, in both trees constructed using concatenated alignments of ribosomal proteins and trees based on gene content, M. kandleri consistently groups with other archaeal methanogens. M. kandleri shares the set of genes implicated in methanogenesis and, in part, its operon organization with Methanococcus jannaschii and Methanothermobacter thermoautotrophicum. These findings indicate that archaeal methanogens are monophyletic. A distinctive feature of M. kandleri is the paucity of proteins involved in signaling and regulation of gene expression. Also, M. kandleri appears to have fewer genes acquired via lateral transfer than other archaea. These features might reflect the extreme habitat of this organism. The sequence is deposited in GenBank under Accession No. AE009439.
IT **406671-25-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanopyrus kandleri AV19 and monophyly of archaeal methanogens)
REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 17 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:385842 CAPLUS
DOCUMENT NUMBER: 135:1234
TITLE: Eicosapentaenoic acid biosynthetic production by recombinant marine cyanobacteria, Synechococcus
INVENTOR(S): Yazawa, Kazuyoshi; Yu, Reiko; Yamada, Akiko; Matsunaga, Sunao; Takeyama, Haruko; Kurane, Ryuichiro
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan; Bioindustry Association; Ministry of Economy, Trade and Industry; National Industrial Research Institute
SOURCE: Jpn. Kokai Tokkyo Koho, 62 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2001145490	A2	20010529	JP 1999-329169	19991119

PRIORITY APPLN. INFO.: JP 1999-329169 19991119
ED Entered STN: 29 May 2001
AB Transformation of marine cyanobacteria with eicosapentaenoic acid (EPA) synthetic enzyme gene cluster for EPA biosynthetic prodn., is disclosed. Plasmid vectors contg. the gene cluster are claimed. The eicosapentaenoic acid (EPA) synthesis gene cluster from an EPA-producing bacterium, Shewanella sp. SCRC-2738, was cloned into a broad-host range vector, pJRD215, and then introduced into a marine cyanobacterium, Synechococcus

sp. NKBG15041c, by conjugation. The transconjugant cyanobacteria produced 3.7 .+-. 0.2% (2.24 .+-. 0.13 mg/L) EPA (n-3) and 2.5 .+-. 0.2% (1.49 .+-. 0.06 mg/L) eicosatetraenoic acid (n-3) of the total fatty acids when the cells were cultured at 23.degree.C at a light intensity of 1,000-1,500 Lx. The EPA and eicosatetraenoic acid contents of the cells were increased to 4.6 .+-. 0.6% (3.86 .+-. 1.11 mg/L) and 4.7 .+-. 0.3% (3.86 .+-. 0.82 mg/L), and 7.5 .+-. 0.3% (1.76 .+-. 0.10 mg/L) and 5.1 .+-. 0.2% (1.19 .+-. 0.06 mg/L) when they were cultured at low temp. (18.degree.C) and at lower light intensity (40 Lx), resp.

IT **342056-52-4P**
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; eicosapentaenoic acid prodn. by recombinant Synechococcus)

L5 ANSWER 18 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:526443 CAPLUS
DOCUMENT NUMBER: 135:87850
TITLE: The complete genome of the crenarchaeon Sulfolobus solfataricus P2
AUTHOR(S): She, Qunxin; Singh, Rama K.; Confalonieri, Fabrice; Zivanovic, Yvan; Allard, Ghislaine; Awayez, Mariana J.; Chan-Weiher, Christina C.-Y.; Clausen, Ib Groth; Curtis, Bruce A.; De Moors, Anick; Erauso, Gael; Fletcher, Cynthia; Gordon, Paul M. K.; Heikamp-De Jong, Ineke; Jeffries, Alex C.; Kozera, Catherine J.; Medina, Nadine; Peng, Xu; Thi-Ngoc, Hoa Phan; Redder, Peter; Schenk, Margaret E.; Theriault, Cynthia; Tolstrup, Niels; Charlebois, Robert L.; Doolittle, W. Ford; Duguet, Michel; Gaasterland, Terry; Garrett, Roger A.; Ragan, Mark A.; Sensen, Christoph W.; Van der Oost, John
CORPORATE SOURCE: Microbial Genome Group, Institute of Molecular Biology, University of Copenhagen, Copenhagen, DK-1307, Den.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(14), 7835-7840
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 22 Jul 2001
AB The genome of the crenarchaeon Sulfolobus solfataricus P2 contains 2,992,245 bp on a single chromosome and encodes 2977 proteins and many RNAs. One-third of the encoded proteins have no detectable homologs in other sequenced genomes. Moreover, 40% appear to be archaeal-specific, and only 12% and 2.3% are shared exclusively with bacteria and eukarya, resp. The genome shows a high level of plasticity with 200 diverse insertion sequence elements, many putative nonautonomous mobile elements, and evidence of integrase-mediated insertion events. There are also long clusters of regularly spaced tandem repeats. Different transfer systems are used for the uptake of inorg. and org. solutes, and a wealth of intracellular and extracellular proteases, sugar, and sulfur-metabolizing enzymes are encoded, as well as enzymes of the central metabolic pathways and motility proteins. The major metabolic electron carrier is not NADH as in bacteria and eukarya but probably ferredoxin. The essential components required for DNA replication, DNA repair and recombination, the cell cycle, transcriptional initiation and translation, but not DNA folding, show a strong eukaryal character with many archaeal-specific features. The results illustrate major differences between crenarchaea and euryarchaea, esp. for their DNA replication mechanism and cell cycle processes and their translational app. The complete annotated genome sequence is available in GenBank Accession No. AE006641.

IT **348670-68-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome of Sulfolobus solfataricus P2)
REFERENCE COUNT: 85 THERE ARE 85 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 19 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:576756 CAPLUS
DOCUMENT NUMBER: 135:163233
TITLE: Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum
AUTHOR(S): Nolling, Jork; Breton, Gary; Omelchenko, Marina V.; Makarova, Kira S.; Zeng, Qiandong; Gibson, Rene; Lee, Hong Mei; Dubois, Joann; Qiu, Dayong; Hitti, Joseph; Wolf, Yuri I.; Tatusov, Roman L.; Sabathe, Fabrice; Doucette-Stamm, Lynn; Soucaille, Philippe; Daly, Michael J.; Bennett, George N.; Koonin, Eugene V.; Smith, Douglas R.; Aldredge, Tyler; Ayers, Mark; Bashirzadeh, Romina; Bochner, Harry; Boivin, Mike; Bross, Susan; Bush, David; Butler, Carole; Caron, Anne; Caruso, Anthony; Cook, Robin; Daggett, Patricia; Deloughery, Craig; Egan, Jeff; Ellston, Dawna; Engelstein, Marcy; Ezedi, Johnny; Gilbert, Katie; Goyal, Anil; Guerin, Jennifer; Ho, Tay; Holtham, Kari; Joseph, Paul; Keagle, Pamela; Kozlovsky, Julia; LaPlante, Mary; LeBlanc, Gary; Lumm, Wendy; Majeski, Amy; McDougall, Steve; Mank, Philip; Mao, Jen-I.; Nocco, Diane; Patwell, Donivan; Phillips, Jonathon; Pothier, Bryan; Prabhakar, Shashi; Richterich, Peter; Rice, Philip; Rosetti, Dawn; Rossetti, Mark; Rubenfield, Marc; Sachdeva, Meena; Snell, Philip; Spadafora, Rob; Spitzer, Lia; Shimer, George; Thomann, Hans-Ulrich; Vicaire, R.; Wall, Kristen; Wang, Ying; Weinstock, Keith; Wong, Lai Peng; Wonsey, A.; Xu, Qinxue; Zhang, Liping
CORPORATE SOURCE: GTC Sequencing Center, Genome Therapeutics Corporation, Waltham, MA, 02453, USA
SOURCE: Journal of Bacteriology (2001), 183(16), 4823-4838
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 09 Aug 2001
AB The genome sequence of the solvent-producing bacterium Clostridium acetobutylicum ATCC 824 was detd. by the shotgun approach. The genome consists of a 3.94-Mb chromosome and a 192-kb megaplasmid that contains the majority of genes responsible for solvent prodn. Comparison of C. acetobutylicum to Bacillus subtilis reveals significant local conservation of gene order, which has not been seen in comparisons of other genomes with similar, or, in some cases closer, phylogenetic proximity. This conservation allows the prediction of many previously undetected operons in both bacteria. However, the C. acetobutylicum genome also contains a significant no. of predicted operons that are shared with distantly related bacteria and archaea but not with B. subtilis. Phylogenetic anal. is compatible with the dissemination of such operons by horizontal transfer. The enzymes of the solventogenesis pathway and of the cellulosome of C. acetobutylicum comprise a new set of metabolic capacities not previously represented in the collection of complete genomes. These enzymes show a complex pattern of evolutionary affinities, emphasizing the role of lateral gene exchange in the evolution of the unique metabolic profile of the bacterium. Many of the sporulation genes identified in B. subtilis are missing in C. acetobutylicum, suggesting

major differences in the sporulation process. Thus, comparative anal. reveals both significant conservation of the genome organization and pronounced differences in many systems that reflect unique adaptive strategies of the two gram-pos. bacteria. The sequence data is available in the GenBank database with Accession Nos. AE001438 and AE007513-AE007868.

IT **353881-58-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence and comparative anal. of the solvent-producing bacterium Clostridium acetobutylicum)

REFERENCE COUNT: 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 20 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:493686 CAPLUS
DOCUMENT NUMBER: 133:115928
TITLE: Schizochytrium polyketide synthase genes and transgenic plants for polyunsaturated long chain fatty acid production
INVENTOR(S): Facciotti, Daniel; Metz, James George; Lassner, Michael
PATENT ASSIGNEE(S): Calgene, LLC, USA
SOURCE: PCT Int. Appl., 303 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000042195	A2	20000720	WO 2000-US956	20000114
WO 2000042195	A3	20000928		
W: BR, CA, IL, JP, MX				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6566583	B1	20030520	US 1999-231899	19990114
CA 2359629	AA	20000720	CA 2000-2359629	20000114
EP 1147197	A2	20011024	EP 2000-904357	20000114
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 2000008760	A	20021008	BR 2000-8760	20000114
JP 2002534123	T2	20021015	JP 2000-593752	20000114

PRIORITY APPLN. INFO.:
US 1999-231899 A 19990114
US 1997-48650P P 19970604
US 1998-90793 A2 19980604
WO 2000-US956 W 20000114

ED Entered STN: 21 Jul 2000
AB The present invention relates to compns. and methods for prepg. polyunsatd. long-chain fatty acids in plants, plant parts and plant cells, such as leaves, roots, fruits and seeds. Nucleic acid sequences and constructs encoding polyketide synthase (PKS)-like genes required for the polyunsatd. long-chain fatty acid prodn., including the genes responsible for eicosapentenoic acid prodn. of Shewanella putrefaciens and novel genes assocd. with the prodn. of docosahexenoic acid in Vibrio marinus are used to generate transgenic plants, plant parts and cells which contain and express one or more transgenes encoding one or more of the PKS-like genes assocd. with such long chain polyunsatd. fatty acid prodn. PKS-like genes from Schizochytrium aggregatum are also provided. Expression of the PKS-like genes in the plant system permits the large scale prodn. of polyunsatd. long-chain fatty acids such as eicosapentenoic acid and docosahexenoic acid for modification of the fatty acid profile of plants,

plant parts and tissues. Manipulation of the fatty acid profiles allows for the prodn. of com. quantities of novel plant oils and products.

IT **153926-89-7**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Schizochytrium polyketide synthase genes and transgenic plants for polyunsatd. long chain fatty acid prodn.)

L5 ANSWER 21 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:754712 CAPLUS
DOCUMENT NUMBER: 133:330538
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302828	AA	20001006	CA 2000-2302828	20000406
EP 1055728	A2	20001129	EP 2000-303770	20000504
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-304161	20000517
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:

US 1999-121825P	P	19990225
US 1999-145918P	P	19990727
US 1999-145951P	P	19990728
US 1999-146386P	P	19990802
US 1999-146388P	P	19990802
US 1999-146389P	P	19990802
US 1999-147038P	P	19990803
US 1999-147204P	P	19990804
US 1999-147302P	P	19990804
US 1999-147192P	P	19990805
US 1999-147260P	P	19990805
US 1999-147303P	P	19990806
US 1999-147416P	P	19990806
US 1999-147493P	P	19990809
US 1999-147935P	P	19990809
US 1999-148171P	P	19990810
US 1999-148319P	P	19990811
US 1999-148341P	P	19990812
US 1999-148565P	P	19990813
US 1999-148684P	P	19990813
US 1999-123180P	P	19990305
US 1999-123548P	P	19990309
US 1999-125788P	P	19990323
US 1999-126264P	P	19990325
US 1999-126785P	P	19990329

US 1999-127462P	P	19990401
US 1999-128234P	P	19990406
US 1999-128714P	P	19990408
US 1999-129845P	P	19990416
US 1999-130077P	P	19990419
US 1999-130449P	P	19990421
US 1999-130510P	P	19990423
US 1999-130891P	P	19990423
US 1999-131449P	P	19990428
US 1999-132048P	P	19990430
US 1999-132407P	P	19990430
US 1999-132484P	P	19990504
US 1999-132485P	P	19990505
US 1999-132486P	P	19990506
US 1999-132487P	P	19990506
US 1999-132863P	P	19990507
US 1999-134256P	P	19990511
US 1999-134218P	P	19990514
US 1999-134219P	P	19990514
US 1999-134221P	P	19990514
US 1999-134370P	P	19990514
US 1999-134768P	P	19990518
US 1999-134941P	P	19990519
US 1999-135124P	P	19990520
US 1999-135353P	P	19990521
US 1999-135629P	P	19990524
US 1999-136021P	P	19990525
US 1999-136392P	P	19990527
US 1999-136782P	P	19990528
US 1999-137222P	P	19990601
US 1999-137528P	P	19990603
US 1999-137502P	P	19990604
US 1999-137724P	P	19990607
US 1999-138094P	P	19990608

ED Entered STN: 26 Oct 2000

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133162185280 necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **303239-85-2 303239-86-3 303239-87-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L5 ANSWER 22 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:776252 CAPLUS
DOCUMENT NUMBER: 134:41140
TITLE: Production of eicosapentaenoic acid by a recombinant marine cyanobacterium, Synechococcus sp.
AUTHOR(S): Yu, Reiko; Yamada, Akiko; Watanabe, Kazuo; Yazawa,

Kazunaga; Takeyama, Haruko; Matsunaga, Tadashi; Kurane, Ryuichiro
CORPORATE SOURCE: Sagami Chemical Research Center, Kanagawa, 229-0012, Japan
SOURCE: Lipids (2000), 35(10), 1061-1064
CODEN: LPDSAP; ISSN: 0024-4201
PUBLISHER: AOCS Press
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 06 Nov 2000
AB The eicosapentaenoic acid (EPA) synthesis gene cluster from an EPA-producing bacterium, Shewanella sp. SCRC-2738, was cloned into a broad-host range vector, pJRD215, and then introduced into a marine cyanobacterium, Synechococcus sp. NKBG15041c, by conjugation. The transconjugant cyanobacteria produced 3.7 .+-. 0.2% (2.24 .+-. 0.13 mg/L) EPA (n-3) and 2.5 .+-. 0.2% (1.49 .+-. 0.06 mg/L) eicosatetraenoic acid (n-3) of the total fatty acids when the cells were cultured at 23.degree.C at a light intensity of 1,000-1,500 Lx. The EPA and eicosatetraenoic acid contents of the cells were increased to 4.6 .+-. 0.6% (3.86 .+-. 1.11 mg/L) and 4.7 .+-. 0.3% (3.86 .+-. 0.82 mg/L), and 7.5 .+-. 0.3% (1.76 .+-. 0.10 mg/L) and 5.1 .+-. 0.2% (1.19 .+-. 0.06 mg/L) when they were cultured at low temp. (18.degree.C) and at lower light intensity (40 Lx), resp.
IT **153926-89-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; eicosapentaenoic acid prodn. by a recombinant Synechococcus sp.)
REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 23 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:66002 CAPLUS
DOCUMENT NUMBER: 128:98584
TITLE: Cloning of genes for 9 eicosapentaenoic acid synthesizing enzymes of Shewanella putrefaciens and expression of the genes in Escherichia coli for production of eicosapentaenoic acid
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kondo, Kiyosi; Kato, Seishi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9801565	A1	19980115	WO 1997-JP2371	19970709
W: AU, CA, JP, NO				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9734583	A1	19980202	AU 1997-34583	19970709
AU 727694	B2	20001221		
EP 913473	A1	19990506	EP 1997-930728	19970709
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
NO 9900083	A	19990304	NO 1999-83	19990108
PRIORITY APPLN. INFO.:			JP 1996-180845 A	19960710
			WO 1997-JP2371 W	19970709

ED Entered STN: 04 Feb 1998
AB Provided is an advantageous process for prodn. of icosapentaenoic acid

(EPA), which process comprises isolation of genes coding for a group of EPA biosynthesis enzymes from Shewanella putrefaciens strain SCRC-2874 and expression of the enzymes in Escherichia coli. Upstream of open reading frame ORF2, downstream of ORF10, and ORF2 are not involved with the biosynthesis of EPA. ORF3, 6, 7, 8, and 9 are essential for the biosynthesis of EPA. EPA is useful as pharmaceuticals, agrochems., foods, and feeds.

IT **153926-89-7**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; cloning of genes for 9 eicosapentaenoic acid synthesizing enzymes of Shewanella putrefaciens and expression of genes in Escherichia coli for prodn. of eicosapentaenoic acid)

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 24 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1996:563418 CAPLUS
DOCUMENT NUMBER: 125:215689
TITLE: Cloning of genes for biosynthetic enzyme group for eicosapentaenoic acid of Shewanella putrefaciens and process for producing eicosapentaenoic acid
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kondo, Kiyosi; Kato, Seishi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 143 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9621735	A1	19960718	WO 1996-JP30	19960112
W: AU, CA, FI, NO				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2209987	AA	19960718	CA 1996-2209987	19960112
AU 9644001	A1	19960731	AU 1996-44001	19960112
JP 08242867	A2	19960924	JP 1996-3485	19960112
EP 831149	A1	19980325	EP 1996-900433	19960112
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				

PRIORITY APPLN. INFO.: JP 1995-4299 19950113
WO 1996-JP30 19960112

ED Entered STN: 21 Sep 1996

AB The gene for enzymes assocd. with the biosynthesis of eicosapentaenoic acid was isolated from Shewanella putrefaciens strain SCRC-2874 and characterized. It contains 9 open reading frames (ORF 2.apprx.10). Manuf. of eicosapentaenoic acid by expression of the genes in transgenic microorganisms such as Escherichia coli is claimed.

IT **153926-89-7**

RL: PRP (Properties)
(amino acid sequence; cloning of genes for biosynthetic enzyme group for eicosapentaenoic acid of Shewanella putrefaciens and process for producing eicosapentaenoic acid)

L5 ANSWER 25 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1995:569921 CAPLUS
DOCUMENT NUMBER: 123:219957
TITLE: The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution
AUTHOR(S): Gompels, U. A.; Nicholas, J.; Lawrence, G.; Jones, M.;

Thomson, B. J.; Martin, M. E. D.; Efstathiou, S.; Craxton, M.; Macaulay, H. A.
CORPORATE SOURCE: Dept. Clinical Sci., London Sch. Hygiene and Tropical Med., London, WC1E 7HT, UK
SOURCE: Virology (1995), 209(1), 29-51
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 24 May 1995
AB The complete DNA sequence was detd. for strain U1102 of human herpesvirus-6, a CD4+ T-lymphotropic virus with disease assocns. in immunodeficient settings and a possible complicating factor in AIDS. The genome is 159,321 bp in size, has a base compn. of 43% G + C, and contains 119 open reading frames. The overall structure is 143 kb bounded by 8 kb of direct repeats, DRL (left) and DRR (right), contg. 0.35 kb of terminal and junctional arrays of human telomere-like simple repeats. Since eight open reading frames are duplicated in the repeats, six span repetitive elements and three are spliced, the genome is considered to contain 102 sep. genes likely to encode protein. The genes are arranged colinearly with those in the genome of the previously sequenced betaherpesvirus, human cytomegalovirus, and has a distinct arrangement of conserved genes relative to the sequenced gammaherpesviruses, herpesvirus saimiri and Epstein-Barr virus, and the alphaherpesviruses, equine herpesvirus-1, varicella-zoster virus, and herpes simplex virus. Comparisons of predicted amino acid sequences allowed the functions of many human herpesvirus-6 encoded proteins to be assigned and showed the closest relation in overall no. and similarity to human cytomegalovirus products, with approx. 67% homologous proteins as compared to the 21% identified in all herpesviruses. The features of the conserved genes and their relative order suggested a general scheme for divergence among these herpesvirus lineages. In addn. to the "core" conserved genes, the genome contains four distinct gene families which may be involved in immune evasion and persistence in immune cells: two have similarity to the "chemokine" chemotactic/proinflammatory family of cytokines, one to their peptide G-protein-coupled receptors, and a fourth to the Ig superfamily.
IT **167975-38-4**
RL: PRP (Properties)
(amino acid sequence; DNA and encoded peptide sequences of human herpesvirus-6)

L5 ANSWER 26 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:184295 CAPLUS
DOCUMENT NUMBER: 120:184295
TITLE: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpesvirus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions
AUTHOR(S): Nicholas, John; Martin, Michelle E. D.
CORPORATE SOURCE: Johns Hopkins Oncol. Cent., Baltimore, MD, 21231, USA
SOURCE: Journal of Virology (1994), 68(2), 597-610
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 16 Apr 1994
AB Human herpesvirus 6 (HHV-6) is prevalent in the human population, with primary infection occurring early in life. Its predominant CD4+ T-lymphocyte tropism, its ability to activate human immunodeficiency virus type 1 (HIV-1) gene expression in vitro, and its upregulation of CD4 expression has led to speculation that HHV-6 may act as a pos. cofactor in the progression of HIV infection to AIDS in individuals infected with both viruses. Previous sequencing studies of restricted regions of the 161.5-kbp genome of HHV-6 have demonstrated unequivocally that it is a

member of the betaherpesvirus subgroup and have indicated that the HHV-6 genome is generally collinear with the unique long (UL) component of human cytomegalovirus (HCMV). This report extended the sequencing studies by detg. the primary structure of 38.5-kbp of the HHV-6 genome (genomic position 21.0 to 59.6 kbp). Within the sequenced region lie 31 open reading frames, 20 of which are homologous to positional counterparts in HCMV. Of particular significance is the identification of homologs of the HCMV UL36-38 and US22-type genes, which have been shown to encode transactivating proteins. DNA sequences encoding these HHV-6 homologs were able to transactivate HIV-1 long terminal repeat-directed chloramphenicol acetyltransferase expression in cotransfection assays, thus demonstrating functional as well as structural conservation of these betaherpesvirus-specific gene products. The data confirm the close relationship between HHV-6 and HCMV and possibly also in the interactions between HHV-6 and HIV in dually infected cells.

IT **153676-37-0**, Genbank L25528-derived protein
RL: PRP (Properties)
(amino acid sequence of)

L5 ANSWER 27 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:211508 CAPLUS
DOCUMENT NUMBER: 120:211508
TITLE: Molecular cloning of gene for eicosapentaenoic acid synthetase group of Shewanella putrefaciens
INVENTOR(S): Yazawa, Kazunaga; Yamada, Akiko; Kato, Seishi; Kondo, Kiyosi
PATENT ASSIGNEE(S): Sagami Chemical Research Center, Japan
SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9323545	A1	19931125	WO 1993-JP641	19930514
W: AU, CA, FI, NO, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2113557	AA	19931125	CA 1993-2113557	19930514
AU 9340881	A1	19931213	AU 1993-40881	19930514
AU 673359	B2	19961107		
JP 06046864	A2	19940222	JP 1993-135133	19930514
EP 594868	A1	19940504	EP 1993-910344	19930514
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
FI 9400203	A	19940314	FI 1994-203	19940114
NO 9400146	A	19940314	NO 1994-146	19940114
PRIORITY APPLN. INFO.:			JP 1992-147945	19920515
			WO 1993-JP641	19930514

ED Entered STN: 30 Apr 1994
AB A gene for eicosapentaenoic acid (I) synthetase group of microorganisms such as Shewanella, Pseudomonas, or Alteromonas can be used for mass prodn. of I by expression of the gene in a host. I is useful as medicine, pesticide, food, feed, etc. A gene encoding I synthetase group was cloned from Shewanella putrefaciens SCRS-2874 using cosmid pWE15 and characterized. Clone pEPA contg. a 37913-base genomic DNA comprised of 8 open reading frames (ORF) was disclosed and the amino acid sequences of each ORF were deduced. Escherichia coli transformed with pEPA was also given.

IT **153926-89-7**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of)

L5 ANSWER 28 OF 33 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:185121 CAPLUS
DOCUMENT NUMBER: 118:185121
TITLE: Manufacture of epitopes of protein p100 of human herpesvirus type 6 for diagnostic or therapeutic uses
INVENTOR(S): Neipel, Frank; Fleckenstein, Bernhard
PATENT ASSIGNEE(S): Behringwerke AG, Germany; Dade Behring Marburg GmbH
SOURCE: Eur. Pat. Appl., 25 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 524421	A1	19930127	EP 1992-110047	19920615
EP 524421	B1	20030326		
R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, PT, SE				
AT 235553	E	20030415	AT 1992-110047	19920615
ES 2194008	T3	20031116	ES 1992-110047	19920615
CA 2073282	AA	19930109	CA 1992-2073282	19920707
AU 9219455	A1	19930114	AU 1992-19455	19920707
AU 666482	B2	19960215		
JP 06113858	A2	19940426	JP 1992-204414	19920708
JP 3425164	B2	20030707		
US 5814475	A	19980929	US 1994-266311	19940627
US 5827519	A	19981027	US 1995-467527	19950606
US 6174685	B1	20010116	US 1995-467528	19950606

PRIORITY APPLN. INFO.: EP 1991-111338 A 19910708
US 1992-908041 B1 19920706
US 1993-126435 B1 19930924
US 1994-266311 A3 19940627

ED Entered STN: 14 May 1993
AB Fragments of the gene for the major capsid protein p100 of human herpesvirus 6 (HHV6) are used to manuf. epitopes for diagnostic differentiation of HHV6 and human cytomegalovirus and for therapeutic applications. The use of the epitope in immunoassays to identify HHV6 infection was demonstrated.
IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6)
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete, manuf. of epitopes of)

L5 ANSWER 29 OF 33 USPATFULL on STN
ACCESSION NUMBER: 2001:7853 USPATFULL
TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA sequences, their preparation and use
INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of
PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6174685	B1	20010116
APPLICATION INFO.:	US 1995-467528		19950606 (8)

RELATED APPLN. INFO.: Division of Ser. No. US 1994-266311, filed on 27 Jun 1994 Continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned Continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ketter, James
ASSISTANT EXAMINER: Yucel, Irem
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 6
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 12 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 333
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further relates to antibodies directed to them and to the corresponding DNA sequences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6)
(amino acid sequence of, complete, manuf. of epitopes of)

L5 ANSWER 30 OF 33 USPATFULL on STN
ACCESSION NUMBER: 1998:131399 USPATFULL
TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA sequences, their preparation and use
INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of
PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5827519		19981027
APPLICATION INFO.:	US 1995-467527		19950606 (8)

RELATED APPLN. INFO.: Division of Ser. No. US 1994-266311, filed on 27 Jun 1994 which is a continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned which is a continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ketter, James
ASSISTANT EXAMINER: Brusca, John S.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 8
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 647
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further relates to antibodies directed to them and to the corresponding DNA sequences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.

IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6)
(amino acid sequence of, complete, manuf. of epitopes of)

L5 ANSWER 31 OF 33 USPATFULL on STN
ACCESSION NUMBER: 1998:118997 USPATFULL
TITLE: Human herpesvirus type 6 protein p100, the corresponding DNA seqences, their preparation and use
INVENTOR(S): Neipel, Frank, Erlangen, Germany, Federal Republic of
Fleckenstein, Bernhard, Wiesenthau, Germany, Federal Republic of
PATENT ASSIGNEE(S): Behring Diagnostics GmbH, Marburg, Germany, Federal Republic of (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5814475		19980929
APPLICATION INFO.:	US 1994-266311		19940627 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1993-126435, filed on 24 Sep 1993, now abandoned which is a continuation of Ser. No. US 1992-908041, filed on 6 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1991-111338	19910708

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Stanton, Brian R.
LEGAL REPRESENTATIVE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 646
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to the human herpesvirus type 6 protein p100 and parts thereof having its specific immunological properties. It further relates to antibodies directed to them and to the corresponding DNA sequences. They can be used in pharmaceutical or diagnostic compositions, optionally together with other HHV-6 proteins or the corresponding DNA sequences.
IT **147156-14-7**, p100 Capsid protein (human herpesvirus 6)
(amino acid sequence of, complete, manuf. of epitopes of)

L5 ANSWER 32 OF 33 MEDLINE on STN DUPLICATE 9
ACCESSION NUMBER: 94025558 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7692666
TITLE: Human herpesvirus-6 glycoprotein H and L homologs are components of the gp100 complex and the gH external domain is the target for neutralizing monoclonal antibodies.
AUTHOR: Liu D X; Gompels U A; Foa-Tomasi L; Campadelli-Fiume G
CORPORATE SOURCE: Department of Medicine, University of Cambridge, United Kingdom.
SOURCE: Virology, (1993 Nov) 197 (1) 12-22.
Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19970203
Entered Medline: 19931122
ABSTRACT:

Previous studies have shown that monoclonal antibody (MAb) 2E4 neutralizes infectivity of human herpesvirus-6 (HHV-6) and also inhibits virus-induced T-lymphocyte syncytia formation. Here we characterize two additional MAbs, 1D3 and 5E7, which have similar properties, and identify the glycoprotein targets. The MAbs could immunoprecipitate and immunofluorescence glycoprotein from both A and B variant strain groups of HHV-6. In reactions with infected cells the MAbs immunoprecipitated a complex of glycoproteins, the "gp100" complex, composed of a major glycoprotein species of 100,000 M(r) and minor components of 80,000 M(r) and 32,000 M(r). We show that the 100,000 M(r) product and most likely the 80,000 M(r) correspond to the HHV-6 homologue of herpes simplex virus-1 (HSV-1) glycoprotein H (gH) while the 32,000 M(r) species corresponds to the glycoprotein L (gL) equivalent. All three MAbs could specifically immunoprecipitate either gH expressed on its own in fibroblasts or a complex of gH and gL co-expressed, but could not immunoprecipitate gL expressed on its own. Consistent with these results, the MAbs could recognize gH in an immunofluorescence assay but not gL. Therefore although the MAbs recognized the complex of glycoproteins, they appeared specific for gH. The HHV-6 glycoproteins were produced in a transient expression system induced by T7-vaccinia virus. Immunoprecipitations were carried out in comparisons with an "epitope-tagged" gH, a recombinant glycoprotein designed to contain at the N-terminus the linear epitope for MAb LP14, raised originally against HSV-1 glycoprotein gD. The epitope-tagged gH was also used as a positive control in determining the domain of HHV-6 gH to which MAbs 2E4, 1D3 and 5E7 were directed. Two gH deletions were constructed, one deleting sequences which may serve as a transmembrane and cytoplasmic anchor domains, the second deleting also part of the external domain. MAb LP14 could immunoprecipitate both HHV-6 gH deletions but the gp100 MAbs recognized only the full-length product or the intact external domain minus the transmembrane and cytoplasmic domains. This indicated the epitopes for these MAbs are contained in the external domain of gH, consistent with the MAbs action in neutralization of virion infectivity and inhibition of virus to cell spread by T-lymphocyte fusion.

CONTROLLED TERM: Check Tags: Comparative Study; Human; Support, Non-U.S. Gov't
Amino Acid Sequence
Animals
*Antibodies, Monoclonal: ME, metabolism
Antigen-Antibody Reactions
Base Sequence
Cell Line
DNA Primers
Electrophoresis, Polyacrylamide Gel
Epitopes: AN, analysis
Fluorescent Antibody Technique
Glycoproteins: IM, immunology
Glycoproteins: IP, isolation & purification
*Glycoproteins: ME, metabolism
Herpesvirus 6, Human: IM, immunology
*Herpesvirus 6, Human: ME, metabolism
Mice
Mice, Inbred BALB C: IM, immunology
Molecular Sequence Data
Molecular Weight
Mutagenesis, Site-Directed
Neutralization Tests
Polymerase Chain Reaction
Sequence Deletion
Sequence Homology, Amino Acid
Transfection
Viral Envelope Proteins: IM, immunology
Viral Envelope Proteins: IP, isolation & purification
*Viral Envelope Proteins: ME, metabolism
Viral Proteins: IM, immunology
Viral Proteins: IP, isolation & purification

*Viral Proteins: ME, metabolism
CAS REGISTRY NO.: 142985-75-9 (glycoprotein H, herpesvirus 6); **147338-03-2 (p100 gene product)**
CHEMICAL NAME: 0 (Antibodies, Monoclonal); 0 (DNA Primers); 0 (Epitopes); 0 (Glycoproteins); 0 (Viral Envelope Proteins); 0 (Viral Proteins)

L5 ANSWER 33 OF 33 MEDLINE on STN
ACCESSION NUMBER: 94018614 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8412672
TITLE: S-layer protein from Thermus thermophilus HB8 assembles into porin-like structures.
AUTHOR: Caston J R; Berenguer J; de Pedro M A; Carrascosa J L
CORPORATE SOURCE: Centro de Biologia Molecular (CSIC-UAM), Universidad Autonoma de Madrid, Cantoblanco Spain.
SOURCE: Molecular microbiology, (1993 Jul) 9 (1) 65-75.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19950206
Entered Medline: 19931104

ABSTRACT:
The cells of the extreme thermophile Thermus thermophilus are surrounded by a regular layer (S-layer) built up by a protein with an apparent molecular mass of 100 kDa (P100). . From purified membrane fractions, three different class of two-dimensional crystals can be obtained by following alternative extractive procedures. One of these crystals, with p6 symmetry, clearly represents the native S-layer detected by freeze etching on whole cells, while the other two, showing p2 and p3 symmetries respectively, closely resemble aggregates of bacterial porins. We demonstrate here by limited proteolysis and Western blotting the surprising fact that the protéin component of the three crystals is the P100 protein. Our biochemical data also show how this protein forms Ca(2+)-stabilized trimers in each crystal, which support the structural analysis that points to p3 units as the common structural block in all of them, and again resembles the situation found in bacterial porins.
CONTROLLED TERM: Check Tags: Support, Non-U.S. Gov't
Blotting, Western
Calcium: ME, metabolism
Cell Fractionation
Crystallization
Edetic Acid: PD, pharmacology
Fourier Analysis
Freeze Etching
Lipids: ME, metabolism
Microscopy, Electron
Peptidoglycan: ME, metabolism
Polymers
*Protein Conformation
Thermus thermophilus: ME, metabolism
*Thermus thermophilus: UL, ultrastructure
*Viral Proteins: CH, chemistry
Viral Proteins: IP, isolation & purification
Viral Proteins: ME, metabolism
CAS REGISTRY NO.: **147338-03-2 (p100 gene product)**; 60-00-4 (Edetic Acid); 7440-70-2 (Calcium)
CHEMICAL NAME: 0 (Lipids); 0 (Peptidoglycan); 0 (Polymers); 0 (Viral Proteins)

=> fil hom
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            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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REFERENCE   1  (residues 1 to 870)
  AUTHORS   Neipel,F., Ellinger,K. and Fleckenstein,B.
  TITLE     Gene for the major antigenic structural protein (p100) of human
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  JOURNAL   J. Virol. 66 (6), 3918-3924 (1992)
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1: BAB17787. mucin [Rattus nor...[gi:11138240] BLink, Domains, Links

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VERSION     BAB17787.1  GI:11138240
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KEYWORDS    .
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (sites)
  AUTHORS   Oinuma,T. and Suganuma,T.
  TITLE     Rat gastric mucin Muc5AC: Sequence of its 5'-region contains
            conserved D-domains and two leucine zipper motifs
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 1851)
  AUTHORS   Oinuma,T., Oinuma,T. and Suganuma,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2000) Tsutomu Oinuma, Miyazaki Medical College,
            Department of Anatomy; Kihara 5200, Kiyotake, Miyazaki 8891692,
            Japan (E-mail:tu@gray.miyazaki-med.ac.jp, Tel:81985851784,
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      841 ecvpgcvcpn glvadgngsc vvaedcpcvh neatyrpget iqvgcnnctc enrmwqctdk
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Apr 13 2004 07:23:25